

OM protein - protein search, using sw model

Run on: April 26, 2003, 13:02:01 ; Search time 23 seconds
(without alignments)

(2902.092 Million cell updates/sec)

Title: US-10-027-000-2

Perfect score: 4391

Sequence: 1 MADIVDEAIIKKLTLAEEKV.....DGVALRQKFTVGETYWNMSGV 833

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubbaa/us08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubbaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubbaa/us06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubbaa/us07_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubbaa/us07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubbaa/us07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubbaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubbaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubbaa/us09_NEW_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubbaa/us09_NEW_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubbaa/us10_NEW_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubbaa/us10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubbaa/us60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubbaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	953	21.7	721	9 US-10-121-032-19
2	951.5	21.7	3782	9 US-09-860-456-4
3	951.5	21.7	3782	9 US-09-988-384B-4
4	951.5	21.7	3782	10 US-09-861-289-4
5	949.5	21.5	809	10 US-09-860-646-24
6	944.5	21.5	809	9 US-09-988-384B-24
7	944.5	21.5	809	10 US-09-861-289-24
8	165	3.8	171	10 US-09-861-289-24
9	151.5	3.5	548	9 US-09-738-626-3855
10	128	2.9	1434	9 US-10-080-05-9
11	126.5	2.9	1394	9 US-10-080-05-9
12	2.8	2609	9 US-10-043-487-383	
13	121	2.8	253	10 US-09-797-662-33
14	118.5	2.7	599	9 US-09-867-767-6
15	118.5	2.7	599	10 US-09-732-350-6
16	115	2.6	1938	9 US-10-014-436-2
17	113.5	2.6	833	9 US-10-014-436-3
18	113.5	2.6	1435	9 US-10-080-505-13
19	2.6	1300	10 US-09-815-242-10906	

RESULT 1

US-10-121-032-19 ; Sequence 19, Application US/10121032 ; Patent No. US200215550A1 ; GENERAL INFORMATION: APPLICANT: Bylina, Edward J. TITLE OF INVENTION: GLYCOSIDASE ENZYMES NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS: ADDRESS: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego STATE: CA COUNTRY: USA ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/121,032
FILING DATE: 09-Apr-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/036,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38-347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid

Sequence 10906, A
Sequence 310, App
Sequence 2, Appl
Sequence 9, Appl
Sequence 7, Appl
Sequence 1197, A
Sequence 5, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 29, Appl
Sequence 45, Appl
Sequence 10438, A
Sequence 2, Appl
Sequence 10, Appl
Sequence 3548, AP
Sequence 12048, A
Sequence 8, Appl
Sequence 579, Ap
Sequence 38, Appl
Sequence 2, Appl

PRIOR FILING DATE: 1999-06-25
; PRIORITY APPLICATION NUMBER: US 09/105,
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 53
; SEQ ID NO: 24
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-988-384B-24

Query Match 21.5%; Score 32.2%; Predicted
Best Local Similarity 32.2%; Predicted
Matches 275; Conservative 112; Mismatches 0

Query	Subject	Score	Length
QY	9 ILKKILTAEKKVLLAGIDFW-----	21.5	809
Db	56 LVAQMTLDEK1SFSV----HWALDPDRQNV	21.5	809
QY	59 VPAACPCGCGTSGLSTFNOTLLEBAGKMMIC	21.5	809
Db	108 QTATALLPAPVALASTFDDTMADSYGVKWMQ	21.5	809
QY	119 GEDPFLAGLAALIRGIOSTGYQATIKIKI	21.5	809
Db	168 SEDPLVSSRRTAYAQIKGQAGLMTTAKI	21.5	809
QY	179 IAVRDSOPGA--FMTAYINGINGVCSENN	21.5	809
Db	228 AS---SKRGAASFMCAVNGNLNGPKSCGNIT	21.5	809
QY	237 VAGLDLEM-----PGPP--RFR	21.5	809
Db	284 TKGLDQEMGVELPGDVPKGEPSPPIAKFFC	21.5	809
QY	283 CAASGYTGENGPEVNTNPEETAAILRKWV	21.5	809
Db	344 GILLATPAPRPE--RDKAGAQASRKV	21.5	809
QY	341 KOATYHGGSAILRAYAYATPFDGLSKQ	21.5	809
Db	401 VDPKVHGIGLSAHVYWPDSAAAPDITKAR	21.5	809
QY	401 RURVFNSEPPGTPNQHQHIDELFFTKIDMH	21.5	809
Db	453 LSPAFNQG-----H	21.5	809
QY	521 YTLKGDTIYPGHGSLRVGGCKVVIDQAE	21.5	809
Db	528 -TISGFAMSATPLSLELGVWTPAAADAT	21.5	809
QY	581 SMKLPGVLDQTLADVAANPNTVVMQTC	21.5	809
Db	584 NISLSPGQDKLISAVADANPNTIVLNTA	21.5	809
QY	641 VEGDYNPSGKLSPEPKRQLDNPAPLNF	21.5	809
Db	644 IKGDVNPSGKLISAVADANPNTIVLNTA	21.5	809
QY	691 ADKDVNPFFGHGLSYTTFAFNSLNSVH-	21.5	809
Db	697 ENVKPLFFGHGLSYTTSFQASPTVVRT	21.5	809
QY	750 AKINRNPVKEIKGFAVELQPEGETKAVTII	21.5	809
Db	757 VTRPQAKKKVKGTVKVSLLAGEAKIVTV	21.5	809
QY	810 SAAKDGVALRGKFTV 824	21.5	809
Db	796 SSAD---LRGSATV 806	21.5	809

RESULT 8
 US-09-734-569-34
 Sequence 34, Application US/09734569
 ; Sequence 34, Application US/09734569
 ; Patent No. US20020054816A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lerchl, Jens
 ; APPLICANT: Renz, Andreas
 ; APPLICANT: Elhardt, Thomas
 ; APPLICANT: Reindl, Andreas
 ; APPLICANT: Bischoff, Friedrich
 ; APPLICANT: Freud, Markus
 ; APPLICANT: Annette
 ; APPLICANT: Duerenig, Elke
 ; APPLICANT: Schmidt, Ralf-Michael
 ; APPLICANT: Reski, Ralf
 ; TITLE OF INVENTION: Moss genes from *Physcomitrella patens* encoding proteins involved
 ; in the synthesis of carbohydrates
 ; TITLE OF INVENTION: In the synthesis of carbohydrates
 ; FILE REFERENCE: BAST-NAF-133-99-US
 ; CURRENT APPLICATION NUMBER: US/09734,569
 ; CURRENT FILING DATE: 2001-03-24
 ; PRIORITY NUMBER: US 60/171, 101
 ; PRIORITY FILING DATE: 1999-12-16
 ; NUMBER OF SEQ ID NOS: 181
 ; NUMBER OF SEQ ID NOS: 181
 ; SEQ ID NO 34
 ; LENGTH: 171
 ; TYPE: PR
 ; ORGANISM: *Physcomitrella patens*
 ; US-09-734-569-34

Query Match 3.8%; Score 165; DB 10; Length 171;
 Best Local Similarity 29.6%; Pred. No. 8.7e-06;
 Matches 56; Conservative 30; Mismatches 65; Indels 38; Gaps 8;

QY 522 TIKGDTIVPGHSLRVGCKVIDQABT-----EKSVALAKEHDQVTCAGLNADWETE 575
 Db 2 TKGDTIL--GGIR---QIGRNSEVYQDNPNSAGYAKKGKFVAIVVGEQPYAENV 54

QY 576 GADRASKMLPGVLDQLIADWAAANPNWVWQMTGTPBEM--PMLDATPAVIQWYGGNET 634
 Db 55 GDNLNLNLPMAPYPAKID--TCSNVACWVWMSGRPLVPEVYGMNAFWAWLPGSE-G 112

QY 635 NSIADWVFGDYNPSGKLSLSPKRLQDNPAALNFRTEBAGRTLYGEDVYVGYYEADK 694
 Db 113 RGVAEVLFQGVNFSGRLSRTRWFRVQDQLP-----MNVGDYY---N 150

QY 695 VNFPEFHGL 703
 Db 151 PLFPFGJGM 159

RESULT 9
 US-09-738-626-3855
 ; Sequence 3855, Application US/09738626
 ; Publication No. US2002019760A1

RESULT 10
 US-10-080-505-9
 ; Sequence 9, Application US/10080505
 ; Publication No. US20030073166A1
 ; GENERAL INFORMATION:
 ; APPLICANT: St. Geme, Joseph W.
 ; TITLE OF INVENTION: *HAEMOPHILUS* ADHERENCE AND PENETRATION PROTEINS
 ; FILE REFERENCE: A-5994-1-RFT/DCP/DHR
 ; CURRENT APPLICATION NUMBER: US/10/080,505
 ; CURRENT FILING DATE: 2002-03-22
 ; PRIORITY NUMBER: US 08/296,791
 ; PRIORITY FILING DATE: 1994-10-25
 ; PRIORITY APPLICATION NUMBER: US 09/839,996
 ; PRIORITY FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 58

RESULT 8
 US-09-734-569-34
 Sequence 34, Application US/09734569
 ; Sequence 34, Application US/09734569
 ; Patent No. US20020054816A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lerchl, Jens
 ; APPLICANT: Renz, Andreas
 ; APPLICANT: Elhardt, Thomas
 ; APPLICANT: Reindl, Andreas
 ; APPLICANT: Bischoff, Friedrich
 ; APPLICANT: Freud, Markus
 ; APPLICANT: Annette
 ; APPLICANT: Duerenig, Elke
 ; APPLICANT: Schmidt, Ralf-Michael
 ; APPLICANT: Reski, Ralf
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIORITY NUMBER: JP 99/377484
 ; PRIORITY FILING DATE: 1999-12-16
 ; PRIORITY APPLICATION NUMBER: JP 00/159162
 ; PRIORITY FILING DATE: 2000-04-07
 ; PRIORITY APPLICATION NUMBER: JP 00/280988
 ; PRIORITY FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 3855
 ; LENGTH: 548
 ; TYPE: PR
 ; ORGANISM: *Corynebacterium glutamicum*
 ; US-09-738-626-3855

Query Match 3.5%; Score 151.5; DB 9; Length 548;
 Best Local Similarity 23.2%; Pred. No. 0.00064; Mismatches 132; Indels 55; Gaps 71; Conservative 48; Mismatches 132; Indels 55; Gaps 71;

QY 64 FPCGTSLSGTNFNQTLLEAERGKMMKCREATAKSAAHVLGLPNTINMORSPLGGRGFFESIGEDPF 123
 Db 188 WPGELGLAALRDAELMETFGTEAKERWARRGGVHKLGYMDLASEPRNSRFNGTGFEGPE 247

QY 124 LASGLGAALRIGQ-----STGVOATIKHF---LCNQDQEDRM---WYQSVITRAIRE 171
 Db 248 LISDYYTAAVVRGLQGPPELSKNSVSTIKHFPGGGVRLDGDHPFHFGQNEYXEDALGK 307

QY 172 IYALPQIAVARDQGPAGTAY-----NGIN-----GVSCENPKYLGCM 211
 Db 308 YHLPPFOAAI-DAGCAGTMYYARPMNNISANQDQLMQNPTQFEEFAVAYNRTFIIDL 366

QY 212 LRKEWGWGLIMSDWYGIYSTTAWVAGLDEMPGPPR-----REGETIKNNSNGKPI 266
 Db 367 LRDAMHGHRGYVNSD---SGVIDAMMWGE-ELSEPERFAAVRAGTDIFSDMANPRLU 421

QY 267 HVI-----DQRAREVQFVKCASAQYEN-----GPETTNTPEVAALRKVGNBG 314
 Db 422 EAVAEHGIDELSNQPVORLLEIFOLGLFENDPVYSEDAEKAIIGAPEVSAALGNAQDLS 481

QY 315 IVALKN 320
 Db 482 VTEILRN 487

QY 84 KMMGKEATAKSA-HVILGPTINNMQRSPIGGROFESIGEDPFLAGGAALTRIGIQSPTGVQ 142 ; Patent No. US20020102276A1
 Db 1486 -LYGDEEVPRSPKPKVLPHTDASKVRAAS- ; GENERAL INFORMATION:
 ; APPLICANT: PEAK, IAN RICHARD ANSELM
 ; ATTORNEY: JENNINGS, MICHAEL PAUL
 QY 143 ATIKHFLCNDQEDRMMYOSTIVTERALRETYALPQTAVRDSDQGAEMTAYNGINGVSCS 202 ;
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0134
 ; CURRENT APPLICATION NUMBER: US09/797,862
 ; PRIORITY APPLICATION NUMBER: PCT/AU98/01031
 ; PRIORITY FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; PRIORITY FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 33
 ; LENGTH: 2353
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-09-797-862-33

Query Match 2-8%; Score 121; DB 10; Length 2353;
 Best Local Similarity 20.8%; Pred. No. 1.8;
 Matches 138; Conservative 92; MissMatches 244; Indels 188; Gaps 35;
 QY 388 GOCCLTPDGAPCMRWRVNEPEGTPNQHDTDEFFKTDML-----VDY----- 432
 Db 1783 TD--NKGDTVTVRY-----APSEAGLHEDMDIRVNHHIPGSPLQFVYDYYNCGHV 1831
 QY 433 -HPKKAADTWADMEGTYTADBCTYE--LGLWVCGTAKAVY----- 471
 Db 1832 AYGP-GLTHGVVNVKPAPEFTVTKDAGEGGSLAIKPGSKAEISCTNDQGTCVSYLPVL 1890
 QY 472 --DDQLVNDATKQVGDAFFGSAARETGRINLVK-GNTYKFKTEFGSAPTYIKGDTI 528
 Db 1891 PDDYSILVVKYHQHVGSPFTRAVGDDSMRMHSHIKVGSADDIPINI-SEPDLSLTAVY 1949
 QY 529 VFGHG-----SLRVGCKVWDDQAEIEKSVALAKEHDQVILCAGLNADWETEGADRA 580
 Db 1950 VPPSGREPCPLKRLRNGHVGISYPKEIGEHLVHVKNQHV-----A 1993
 QY 581 SKMLPGVLDQL-TADYAAANPNTVVMQTPPEENPWLDTAPAVIQAWYGG----- 630
 Db 1994 SPPIPVVISQSEIGDASRVRVSGOGLHEGTFPEAFIDIR--DAGIGGLSIEGPS 2050
 QY 631 -----NETGNISIADYVGDFDNPCK----- 650
 Db 2051 KWDINTEDLEDGETCRVTCPEPGNYTINKFADODHVGSPSPSVKVTGBGRVKSITRR 2110
 QY 651 -----LSUSFKP-RQDNPAFL--NFRTEAGRLYGED----- 680
 Db 2111 RAPSVAVGSHCDLSKIPETISIQDMAQTSPSKTHEAIVEGENHHTYCIREVPAEMG 2170
 QY 681 --VYVGYRITYEADKDVN--PFGHGSYTTA-----FS----- 711
 Db 2171 THTVSKYKQHVGSPFQFTVPIGEGGAKHVKRAGGPFOLERAZAGVFAEFSWTREAGA 2230
 QY 712 -NLSVS-----HKGDKLVSLSVSKVING-----SVP 735
 Db 2231 GGLATAVEGPKSAETSFEDRKDKSGCGVAYWQERGDYEVSVKPNEEHIFDSPTPVVPVASP 2290
 QY 736 GAQVAKOLYVKPLQAA-KINRPVK--EJKGF---AKVELQPG--ETKAVTIEQPKY 783
 Db 2291 SGDARRLTWVSSLQESGLKVNQPAFASVSLNGAKGAIKAVHSPGALBECYVIEIDQKY 2350
 QY 784 VAYVDEERQWCVF 798
 Db 2351 AVRFIPRENGVYIID 2365.

RESULT 13
 US-09-797-862-33
 ; Sequence 33, Application US/09797862

RESULT 14
 US-09-869-877-6
 ; Sequence 6, Application US/09869877
 ; Publication No. US20020192792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schneider, Palle
 ; APPLICANT: Danielsen, Steffen
 ; TITLE OF INVENTION: Laccaze Mutants
 ; FILE REFERENCE: 10179.204 US
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 599
 ; TYPE: PRY
 ; ORGANISM: Rhizoctonia solani
 ; US-09-869-877-6

Query Match 2.7%; Score 118.5; DB 9; Length 599;
 Best Local Similarity 20.9%; Pred. No. 0.36; Gaps 29;
 Matches 122; Conservative 75; Mismatches 223; Indels 163; Gaps 29;

QY 257 FNVSNKGPFIFHVIDQRAREVLOFVKKCAASGVTEENGPETVNNTPETAALLRKVGNEGIV 316
 Db 26 FDVANG-----AVAPDGVTN-----AVLVNGRFPGPL 53

QY 317 LLKNNENVLPLSKKKTLIVGPNQAKQT--YHGGSAALRAYAVTPFDGLSKOLETPP 373
 Db 54 ITANKGDTLKVTRNK--LSDPTMRSTITHWKG---LLOHRTAEDGAFVTOCPIPP 107

QY 374 -SYTGVAYTVPPLGEC-----LTPDGAPGMWRVFNEPGTPNQHIDELFT 423
 Db 108 QESVTY---TMP---LGEOTGTYWVHSHLSQYDGLRGPTVYDHPYRNVD-VDDE 160

QY 424 KTDMLVDYHPKAADTWADMEGYTADECTYELGLWVCGTAKAYDDLVNDATQ 483
 Db 161 RTVFTLADWYH-----TPSEALIATHDVLKTIPDGTNGKGY 199

QY 484 VPGDAFGSATRETRGTRNVLVKGNTYKFKIEGGSAPTYTLKGDTIVPGHSSLRVSGCKVI 543
 Db 200 DPASANTNTILENLYTIVKKGKRYKLRLINASATASFRFG---VQGH---KCTII 250

QY 544 DDAEAEKSVALAKEHDQVITCAG-----LNADETEGDRASMKLPGVLDQHIDELFT 597
 Db 251 EADGVLTJKPI---EVADFIDLAGORYSCTIKAD---QDPSYWINAP---ITNVLN 297

QY 598 ANPNTVVMQTC-TPEEMP-----LDAPIVQW-----YGGNETG----- 634
 Db 298 TNYOALLYVYEDDRKRPTHWPKFELTWKISNEITIOWQHKSHGKGKHHKVRAGGV 357

QY 635 NSTADVVFGDYNSPGKSLISPFKRLQDNPAFTNFR-TEAGRTRLYGEDVYV----- 683
 Db 358 SGLSSRKVRSASLDSKKAVALAALVAGEAEELDKRQEDNSTDVLDETKLIPVQGAPG 417

QY 684 GYYVEEFADKDVNPFGHLSYT---EAFSNLUSVSHKD-----GKLSV--LSV 728
 Db 418 GSR---PADVVVPLDEGLNFKANGLTINNYSYSPDVPFLKLTDKDKDASDFTAD 472

RESULT 15
 US-09-732-350-6
 ; Sequence 6, Application US/09732350
 ; Patient No. US2001031490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Xu, Feng

Query Match 2.7%; Score 118.5; DB 10; Length 599;
 Best Local Similarity 20.9%; Pred. No. 0.36; Gaps 29;
 Matches 122; Conservative 75; Mismatches 223; Indels 163; Gaps 29;

QY 257 FNVSNKGPFIFHVIDQRAREVLOFVKKCAASGVTEENGPETVNNTPETAALLRKVGNEGIV 316
 Db 26 FDVANG-----AVAPDGVTN-----AVLVNGRFPGPL 53

QY 317 LLKNNENVLPLSKKKTLIVGPNQAKQT--YHGGSAALRAYAVTPFDGLSKOLETPP 373
 Db 54 ITANKGDTLKVTRNK--LSDPTMRSTITHWKG---LLOHRTAEDGAFVTOCPIPP 107

QY 374 -SYTGVAYTVPPLGEC-----LTPDGAPGMWRVFNEPGTPNQHIDELFT 423
 Db 108 QESVTY---TMP---LGEOTGTYWVHSHLSQYDGLRGPTVYDHPYRNVD-VDDE 160

QY 424 KTDMLVDYHPKAADTWADMEGYTADECTYELGLWVCGTAKAYDDLVNDATQ 483
 Db 161 RTVFTLADWYH-----TPSEALIATHDVLKTIPDGTNGKGY 199

QY 484 VPGDAFGSATRETRGTRNVLVKGNTYKFKIEGGSAPTYTLKGDTIVPGHSSLRVSGCKVI 543
 Db 200 DPASANTNTILENLYTIVKKGKRYKLRLINASATASFRFG---VQGH---KCTII 250

QY 544 DDAEAEKSVALAKEHDQVITCAG-----LNADETEGDRASMKLPGVLDQHIDELFT 597
 Db 251 EADGVLTJKPI---EVADFIDLAGORYSCTIKAD---QDPSYWINAP---ITNVLN 297

QY 598 ANPNTVVMQTC-TPEEMP-----LDAPIVQW-----YGGNETG----- 634
 Db 298 TNYOALLYVYEDDRKRPTHWPKFELTWKISNEITIOWQHKSHGKGKHHKVRAGGV 357

QY 635 NSTADVVFGDYNSPGKSLISPFKRLQDNPAFTNFR-TEAGRTRLYGEDVYV----- 683
 Db 358 SGLSSRKVRSASLDSKKAVALAALVAGEAEELDKRQEDNSTDVLDETKLIPVQGAPG 417

QY	684	GYRYVFSEADKVNFEPFGHGLSYTT--FAFSNL-SVSHD-----GKLSVS--LSV	728
Db	418	GSR----PAPVWVPLDFGNEFANGLWINTNNVSYSPPDVPPRLKILTDKDVDASETAD	472
QY	729	KNTGSVPQAVQALYYVKPLQAQAKINRPPVKEKLGFAKVVELPQCE	771
Db	473	EHTYIUPKQVVELHKG-QAIGIVPL-HLHGHPDQVQFGD	513

Search completed: April 26, 2003, 13:07:00
Job time : 37 secs